

Please also amend the specification by deleting Sequence Submission pp. 84-110,
and substitute therefore the attached Sequence Submission, pp. 84-108.

REMARKS

The amendments to the related application section provide the filing dates for the individual priority applications from which this application claims benefit.

The amendments to the sequence listing correct various formalities in the originally filed listing of the parent application. No new matter is added thereby.


The Applicants also attach a request under 37 C.F.R. § 1.821(e) that the computer-readable form filed in the parent Application No. 09/351,777 be used as the computer-readable form for the instant application.

I hereby state that the informational contents of the paper and computer readable copies of the above Sequence Listing are believed to be the same. This submission involves no new matter as the enclosed sequences are the same as those filed in the priority documents.

CONCLUSION

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,


Frank J. Mycroft
Reg. No. 46,946

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
Tel: (415) 576-0200
Fax: (415) 576-0300
FJM:meg
SF 1215778 v1

ERIN E. MURPHY, JANE D. MATTSON,
ELIZABETH ESTHER MARY BATES,
DANIEL M. GORMAN and SERGE J.E.
LEBECQUE

PATENT

Application No.:
Page 3

VERSION WITH MARKINGS TO SHOW CHANGES

In the Specification:

This application is a Continuation Application of U.S. Patent Utility Application No. 09/351,777 filed on July 12, 1999. USSN 09/351,777 was a conversion to a U.S. Utility Patent Application of U.S. Provisional Patent Application of USSN 60/092,658 which was filed on July 13, 1998; USSN 60/093,897 which was filed on July 23, 1998; and USSN 60/099,999 which was filed on September 11, 1998. This application incorporates herein by reference, and claims priority to, each of these four applications. [This filing is a conversion to a U.S. Utility Patent Application of U.S. Provisional Patent Applications USSN 60/092,658; USSN 60/093,897; and USSN 60/099,999; each of which is incorporated herein by reference].

SEQUENCE SUBMISSION

SubA2

5 SEQ ID NO: 1 is a primate HDTEA84 nucleic acid sequence.
SEQ ID NO: 2 is a primate HDTEA84 amino acid sequence.
SEQ ID NO: 3 is a primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 4 is a primate HSLJD37R amino acid sequence.
SEQ ID NO: 5 is supplemented primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 6 is supplemented primate HSLJD37R amino acid sequence.
10 SEQ ID NO: 7 is variant primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 8 is variant primate HSLJD37R amino acid sequence.
SEQ ID NO: 9 is murine TNF-R2 amino acid sequence.
SEQ ID NO: 10 is human TNF-R2 amino acid sequence.
SEQ ID NO: 11 is human OPG amino acid sequence.
15 SEQ ID NO: 12 is a rodent RANKL nucleic acid sequence.
SEQ ID NO: 13 is a rodent RANKL amino acid sequence.
SEQ ID NO: 14 is a primate RANKL nucleic acid sequence.
SEQ ID NO: 15 is a primate RANKL amino acid sequence.
SEQ ID NO: 16 is another primate RANKL nucleic acid sequence.
SEQ ID NO: 17 is another primate RANKL amino acid sequence.
20 SEQ ID NO: 18 is a variant primate RANKL nucleic acid sequence.
SEQ ID NO: 19 is a variant primate RANKL amino acid sequence.

<110> Murphy, Erin E.
Mattson, Jeanine D.
25 Bates, Elizabeth Esther Mary
Gorman, Daniel M.
Lebecque, Serge J.E.

<120> Mammalian Genes; Related Reagents

30 <130> SF0818K

<140>

<141>

35 <160> 19

<170> PatentIn Ver. 2.0

40 <210> 1
<211> 1137
<212> DNA
<213> primate

45 <220>
<221> CDS
<222> (99)..(998)

50 <220>
<221> misc_feature
<222> (367)
<223> W; may be A or T; translated amino acid depends on genetic code

55 <220>
<221> mat_peptide
<222> (132)..(998)

<400> 1
cgcaggcgga cccgggggcaa aggaggtggc atgtcgggtca ggcacagcag ggtcctgtgt 60

SubA2

MURPHY, et al.

85

SF0818K

	ccgcgctgag ccgcgctctc cctgctccag caaggacc atg agg gcg ctg gag ggg	116
	Met Arg Ala Leu Glu Gly	
	-10	
5	cca ggc ctg tgg ctg ctg tgc ctg gtg ttg gcg ctg cct gcc ctg ctg	164
	Pro Gly Leu Ser Leu Leu Cys Leu Val Leu Ala Leu Pro Ala Leu Leu	
	-5 -1 1 5 10	
10	ccg gtg ccg gct gta cgc gga gtg gca gaa aca ccc acc tac ccc tgg	212
	Pro Val Pro Ala Val Arg Gly Val Ala Glu Thr Pro Thr Tyr Pro Trp	
	15 20 25	
15	cgg gac gca gag aca ggg gag cgg ctg gtg tgc gcc cag tgc ccc cca	260
	Arg Asp Ala Glu Thr Gly Glu Arg Leu Val Cys Ala Gln Cys Pro Pro	
	30 35 40	
20	ggc acc ttt gtg cag cgg ccg tgc cgc cga gac agc ccc atg acg tgt	308
	Gly Thr Phe Val Gln Arg Pro Cys Arg Arg Asp Ser Pro Met Thr Cys	
	45 50 55	
25	ggc ccg tgt cca ccg cgc cac tac acg cag ttc tgg aac tac ctg gag	356
	Gly Pro Cys Pro Pro Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu	
	60 65 70 75	
30	cgc tgc cgc twc tgc tac gtc ctc tgc ggg gag cgt gag gag gag gca	404
	Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly Glu Arg Glu Glu Glu Ala	
	80 85 90	
35	cgg gct tgc cac gcc acc cac aac cgt gcc tgc cgc tgc cgc acc ggc	452
	Arg Ala Cys His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly	
	95 100 105	
40	ttc ttc gcg cac gct ggt ttc tgc ttg gag cac gca tgc tgt cca cct	500
	Phe Phe Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro	
	110 115 120	
45	ggt gcc ggc gtg att gcc ccg ggc acc ccc agc cag aac acg cag tgc	548
	Gly Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys	
	125 130 135	
50	cag ccg tgc ccc cca ggc acc ttc tca gcc agc agc tcc agc tca gag	596
	Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser Glu	
	140 145 150 155	
55	cag tgc cag ccc cac cgc aac tgc acg gcc ctg ggc ctg gcc ctc aat	644
	Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala Leu Asn	
	160 165 170	
60	gtg cca ggc tct tcc tcc cat gac acc ctg tgc acc agc tgc act ggc	692
	Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser Cys Thr Gly	
	175 180 185	
65	ttc ccc ctc agc acc agg gta cca gga gct gag gag tgt gag cgt gcc	740
	Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu Cys Glu Arg Ala	
	190 195 200	
70	gtc atc gac ttt gtg gct ttc cag gac atc tcc atc aag agg ctg cag	788
	Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser Ile Lys Arg Leu Gln	
	205 210 215	

SubA2

MURPHY, et al.

86

SF0818K

5 cgg ctg ctg cag gcc ctc gag gcc ccg gag ggc tgg ggt ccg aca cca 836
Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu Gly Trp Gly Pro Thr Pro
220 225 230 235

10 agg gcg ggc cgc gcg gcc ttg cag ctg aag ctg cgt cgg cgg ctc acg 884
Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys Leu Arg Arg Arg Leu Thr
240 245 250

15 gag ctc ctg ggg gcg cag gac ggg gcg ctg ctg gtg cgg ctg ctg cag 932
Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu Leu Val Arg Leu Leu Gln
255 260 265

20 gcg ctg cgc gtg gcc agc atg ccc ggg ctg gag cgg agc gtc cgt gag 980
Ala Leu Arg Val Ala Arg Met Pro Gly Leu Glu Arg Ser Val Arg Glu
270 275 280

25 cgc ttc ctc cct gtg cac tgatcctggc cccctcttat ttattctaca 1028
Arg Phe Leu Pro Val His
285

30 tccttggcac cccacttgca ctgaaagagg ctttttttta aatagaagaa atgaggtttc 1088
ttaaagctta tttttataaa gctttttcat aaaaaaaaaa aaaaaaaaaa 1137

35 <210> 2
<211> 300
<212> PRT
<213> primate

40 <400> 2
Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val Leu
-10 -5 -1 1 5

45 Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val Ala Glu
10 15 20

50 Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu Arg Leu Val
25 30 35

55 Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg Pro Cys Arg Arg
40 45 50

60 Asp Ser Pro Met Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln
55 60 65

65 Phe Trp Asn Tyr Leu Glu Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly
70 75 80 85

70 Glu Arg Glu Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala
90 95 100

75 Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu
105 110 115

80 His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro
120 125 130

85 Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala

Sub A2

135 140 145

Ser Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala
150 155 160 165

5 Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu
170 175 180

10 Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala
185 190 195

Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile
200 205 210

15 Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
215 220 225

Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys
230 235 240 245

20 Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu
250 255 260

25 Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met Pro Gly Leu
265 270 275

Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
280 285

30 <210> 3
<211> 1031
<212> DNA
<213> primate

35 <220>
<221> CDS
<222> (402)..(1031)

40 <220>
<221> mat_peptide
<222> (525)..(1031)

45 <220>
<221> misc_feature
<222> (2)
<223> N at 2 or 9; may be A, C, G, or T

50 <220>
<221> misc_feature
<222> (664)
<223> K; may be G or T; translated amino acid depends on genetic code

55 <220>
<221> misc_feature
<222> (956)
<223> N at 956 and 8989 may be A, C, G, or T; translated amino acid
depends on genetic code

60

SubA2

MURPHY, et al.

88

SF0818K

<400> 3
cngactcant cccctgccga ccagctctggg cagcggagga ggggtggttg cagtggctgg 60
aagcttcgct atgggaagtc gttcctttgc tctctcgcgc ccagtcctcc tccctgggtc 120
5 tcttcagccg ctgtcggagg agagcaccgc gagacgcggg ctgcagtcgc ggcggcttct 180
ccccgcctgg ggcggccgcgc cgctgggcag gtgctgagcg cccctagagc ctcccttgcc 240
10 gcctccctcc tctgcocggc cgcagcagtg cacatggggg gttggaggta gatgggctcc 300
cggccccgga ggcggcgggt gatgcggcgc tgggcagaag cagccgccga ttccagctgc 360
15 cccgcgcgcc cggggcgccc ctgcgagtc cgggttcagc c atg ggg acc tct ccg 416
Met Gly Thr Ser Pro
-40
agc agc agc acc gcc ctc gcc tcc tgc agc cgc atc gcc cgc cga gcc 464
20 Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg Ile Ala Arg Arg Ala
-35 -30 -25
aca gcc acg atg atc gcg ggc tcc ctt ctc ctg ctt gga ttc ctt agc 512
25 Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu Leu Gly Phe Leu Ser
-20 -15 -10 -5
acc acc aca gct cag cca gaa cag aag gcc tcg aat ctc att ggc aca 560
30 Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser Asn Leu Ile Gly Thr
-1 1 5 10
tac cgc cat gtt gac cgt gcc acc ggc cag gtg cta acc tgt gac aag 608
35 Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val Leu Thr Cys Asp Lys
15 20 25
tgt cca gca gga acc tat gtc tct gag cat tgt acc aac aca agc tgc 656
40 Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys Thr Asn Thr Ser Cys
30 35 40
gcg tct gkc agc agt tgc cct gtg ggg acc ttt acc agg cat gag aat 704
45 Ala Ser Xaa Ser Ser Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn
45 50 55 60
ggc ata gag aaa tgc cat gac tgt agt cag cca tgc cca tgg cca atg 752
50 Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met
65 70 75
att gag aaa tta cct tgt gct gcc ttg act gac cga gaa tgc act tgc 800
55 Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys
80 85 90
cca cct ggc atg ttc cag tct aac gct acc tgt gcc ccc cat acg gtg 848
60 Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His Thr Val
95 100 105
tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg aca gag act gag gat 896
110 115 120
gtg cgg tgt aag cag tgt gct cgg ggg tac ttc tca gat gtg cct tct 944
125 130 135 140
Val Arg Cys Lys Gln Cys Ala Arg Gly Tyr Phe Ser Asp Val Pro Ser

SubA2

MURPHY, et al.

89

SF0818K

agt gtg atg aan gca aag cat aca cag act gtc tgg atc aga acn tgg 992
Ser Val Met Xaa Ala Lys His Thr Gln Thr Val Trp Ile Arg Xaa Trp
145 150 155

5 ttg gtg atc aag ccg ggg gga cca agg aga cag aca act 1031
Leu Val Ile Lys Pro Gly Gly Pro Arg Arg Gln Thr Thr
160 165

10 <210> 4
<211> 210
<212> PRT
<213> primate

15 <400> 4
Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

20 Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25 -20 -15 -10

Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
-5 -1 1 5

25 Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20

30 Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
25 30 35

Thr Asn Thr Ser Cys Ala Ser Xaa Ser Ser Cys Pro Val Gly Thr Phe
40 45 50 55

35 Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
75 80 85

40 Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
90 95 100

45 Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
105 110 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Tyr Phe
120 125 130 135

50 Ser Asp Val Pro Ser Ser Val Met Xaa Ala Lys His Thr Gln Thr Val
140 145 150

Trp Ile Arg Xaa Trp Leu Val Ile Lys Pro Gly Gly Pro Arg Arg Gln
155 160 165

55 Thr Thr

60 <210> 5

SWP2

MURPHY, et al.

90

SF0818K

<211> 2877
<212> DNA
<213> primate

5 <220>
<221> CDS
<222> (410)..(2374)

10 <220>
<221> mat_peptide
<222> (533)..(2374)

15 <400> 5
ggcagagcc gactcagtc ctcgccgacc agtctgggca gcggaggagg gtggttggca 60
gtggttgga gcttcgctat gggaagtctg tctttgtct tctcgcgccc agtcctctc 120
cctggttctc ctcagccgct gtggaggag agcaccgga gacgcgggct gcagtcgcgg 180
20 cggtttctcc ccgectgggc ggccgcgccc ctgggcaggt gctgagcgcc cctagcgcc 240
cccttgccgc ctccctctc tgcccggccg cagcagtga catgggggtgt tggaggtaga 300
tgggctccc gcccgggagg cggcggtgga tgcggcgctg ggcagaagca gccgccgatt 360
25 ccagctgcc cgcgcgcccc gggcgcccc ggcagtcgcc gggtcagcc atg ggg acc 418
Met Gly Thr
-40

30 tct ccg agc agc agc acc gcc ctc gcc tcc tgc agc cgc atc gcc cgc 466
Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg Ile Ala Arg
-35 -30 -25

35 cga gcc aca gcc acg atg atc gcg gcc tcc ctt ctc ctg ctt gga ttc 514
Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu Leu Gly Phe
-20 -15 -10

40 ctt agc acc acc aca gct cag cca gaa cag aag gcc tgc aat ctc att 562
Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser Asn Leu Ile
-5 -1 1 5 10

45 ggc aca tac cgc cat gtt gac cgt gcc acc gcc cag gtg cta acc tgt 610
Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val Leu Thr Cys
15 20 25

50 gac aag tgt cca gca gga acc tat gtc tct gag cat tgt acc aac aca 658
Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys Thr Asn Thr
30 35 40

55 agc ctg cgc gtc tgc agc agt tgc cct gtg ggg acc ttt acc agg cat 706
Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe Thr Arg His
45 50 55

60 gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca tgc cca tgg 754
Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys Pro Trp
60 65 70

65 cca atg att gag aaa tta cct tgt gct gcc ttg act gac cga gaa tgc 802
Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys
75 80 85 90

act tgc cca cct ggc atg ttc cag tct aac gct acc tgt gcc ccc cat 850
Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His
95 100 105

5 acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg aca gag act 898
Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr
110 115 120

10 gag gat gtg cgg tgt aag cag tgt gct cgg ggt acc ttc tca gat gtg 946
Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser Asp Val
125 130 135

15 cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt ctg agt cag 994
Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys Leu Ser Gln
140 145 150

20 aac ctg gtg gtg atc aag ccg ggg acc aag gag aca gac aac gtc tgt 1042
Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn Val Cys
155 160 165 170

25 ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc cct ggc aca 1090
Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser Pro Gly Thr
175 180 185

30 gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa gtc cct tcc 1138
Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu Val Pro Ser
190 195 200

35 tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc aac tct tct 1186
Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser Asn Ser Ser
205 210 215

40 gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa ggg aca gtc 1234
Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu Gly Thr Val
220 225 230

45 cct gac aac aca agc tca gca agg ggg aag gaa gac gtg aac aag acc 1282
Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val Asn Lys Thr
235 240 245 250

50 ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc cac cac aga 1330
Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro His His Arg
255 260 265

55 cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg ggc gag aag 1378
His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly Gly Glu Lys
270 275 280

60 tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct aga cag aac 1426
Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro Arg Gln Asn
285 290 295

cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg atg att gtg 1474
Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp Met Ile Val
300 305 310

ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg gtg tgc agt atc cgg 1522
Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys Ser Ile Arg
315 320 325 330

aaa agc tgc agg act ctg aaa aag ggg ccc cgg cag gat ccc agt gcc	1570
Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala	
335 340 345	
att gtg gaa aag gca ggg ctg aag aaa tcc atg act cca acc cag aac	1618
Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn	
350 355 360	
cgg gag aaa tgg atc tac tac tgc aat ggc cat ggt atc gat atc ctg	1666
Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu	
365 370 375	
aag ctt gta gca gcc caa gtg gga agc cag tgg aaa gat atc tat cag	1714
Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	
380 385 390	
ttt ctt tgc aat gcc agt gag agg gag gtt gct gct ttc tcc aat ggg	1762
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn Gly	
395 400 405 410	
tac aca gcc gac cac gag cgg gcc tac gca gct ctg cag cac tgg acc	1810
Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His Trp Thr	
415 420 425	
atc cgg ggc ccc gag gcc agc ctc gcc cag cta att agc gcc ctg cgc	1858
Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser Ala Leu Arg	
430 435 440	
cag cac cgg aga aac gat gtt gtg gag aag att cgt ggg ctg atg gaa	1906
Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg Gly Leu Met Glu	
445 450 455	
gac acc acc cag ctg gaa act gac aaa cta gct ctc ccg atg agc ccc	1954
Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala Leu Pro Met Ser Pro	
460 465 470	
agc ccg ctt agc ccg agc ccc atc ccc agc ccc aac gcg aaa ctt gag	2002
Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro Asn Ala Lys Leu Glu	
475 480 485 490	
aat tcc gct ctc ctg acg gtg gag cct tcc cca cag gac aag aac aag	2050
Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro Gln Asp Lys Asn Lys	
495 500 505	
ggc ttc ttc gtg gat gag tgc gag ccc ctt ctc cgc tgt gac tct aca	2098
Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu Arg Cys Asp Ser Thr	
510 515 520	
tcc agc ggc tcc tcc gcg ctg agc agg aac ggt tcc ttt att acc aaa	2146
Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly Ser Phe Ile Thr Lys	
525 530 535	
gaa aag aag gac aca gtg ttg cgg cag gta cgc ctg gac ccc tgt gac	2194
Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg Leu Asp Pro Cys Asp	
540 545 550	
ttg cag cct atc ttt gat gac atg ctc cac ttt cta aat cct gag gag	2242
Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe Leu Asn Pro Glu Glu	
555 560 565 570	

Sub A2

MURPHY, et al.

93

SF0818K

ctg cgg gtg att gaa gag att ccc cag gct gag gac aaa cta gac cgg 2290
Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg
575 580 585

cta ttc gaa att att gga gtc aag agc cag gaa gcc agc cag acc ctc 2338
Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu
590 595 600

ctg gac tct gtc tat agc cat ctt cct gac ctg ctg tagaacaatag 2384
Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu
605 610

ggatactgca ttctggaaat tactcaattt agtggcaggg tggtttttta atttccttct 2444

gtgtctgatt ttgtttgttt ggggtgtgtg tgtgtgtttg tgtgtgtgtg tgtgtgtgtg 2504

tgtgtgtgtg tttaacagag aatatggcca gtgcttgagt tctttctcct tctctctctc 2564

tctttttttt ttaaataact cttctgggaa gttggtttat aagcctttgc caggtgtaac 2624

tggtgtgaaa taccaccac taaagttttt taagtccat attttctcca ttttgcttctc 2684

ttatgtattt tcaagattat tctgtgcact ttaaatttac tcaacttacc ataatgcag 2744

tgtgactttt cccacacact ggattgtgag gctcttaact tcttaaaagt ataatggcat 2804

cttgatgaatc ctataagcag tctttatgtc tcttaacatt cacacctact ttttaaaaac 2864

aaatattatt act 2877

<210> 6

<211> 655

<212> PRT

<213> primate

<400> 6

Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25 -20 -15 -10

Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
-5 -1 1 5

Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
25 30 35

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
40 45 50 55

Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp

Subs

MURPHY, et al.

94

SF0818K

	75	80	85
5	Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys 90 95 100		
10	Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly 105 110 115		
15	Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe 120 125 130 135		
20	Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys 140 145 150		
25	Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp 155 160 165		
30	Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser 170 175 180		
35	Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu 185 190 195		
40	Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser 200 205 210 215		
45	Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu 220 225 230		
50	Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val 235 240 245		
55	Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro 250 255 260		
60	His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly 265 270 275		
	Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro 280 285 290 295		
	Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp 300 305 310		
	Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys 315 320 325		
	Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp 330 335 340		
	Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro 345 350 355		
	Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile 360 365 370 375		
	Asp Ile Leu Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp 380 385 390		
	Ile Tyr Gln Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe		

SubA2

MURPHY, et al.

95

SF0818K

395 400 405

5 Ser Asn Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln
410 415 420

10 His Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser
425 430 435

15 Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg Gly
440 445 450 455

20 Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala Leu Pro
460 465 470

25 Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro Asn Ala
475 480 485

30 Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro Gln Asp
490 495 500

35 Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu Arg Cys
505 510 515

40 Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly Ser Phe
520 525 530 535

45 Ile Thr Lys Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg Leu Asp
540 545 550

50 Pro Cys Asp Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe Leu Asn
555 560 565

55 Pro Glu Glu Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu Asp Lys
570 575 580

60 Leu Asp Arg Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser
585 590 595

Gln Thr Leu Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu
600 605 610

<210> 7
<211> 1474
<212> DNA
<213> primate

<220>
<221> CDS
<222> (1)..(1332)

<220>
<221> mat_peptide
<222> (124)..(1332)

<400> 7
atg ggg acc tct ccg agc agc agc acc gcc ctc gcc tcc tgc agc cgc 48
Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

SubA27

MURPHY, et al.

96

SF0818K

	atc gcc cgc cga gcc aca gcc acg atg atc gcg ggc tcc ctt ctc ctg	96
	Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu	
	-25 -20 -15 -10	
5	ctt gga ttc ctt agc acc acc aca gct cag cca gaa cag aag gcc tcg	144
	Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser	
	-5 -1 1 5	
10	aat ctc att ggc aca tac cgc cat gtt gac cgt gcc acc ggc cag gtg	192
	Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val	
	10 15 20	
15	cta acc tgt gac aag tgt cca gca gga acc tat gtc tct gag cat tgt	240
	Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys	
	25 30 35	
20	acc aac aca agc ctg cgc gtc tgc agc agt tgc cct gtg ggg acc ttt	288
	Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe	
	40 45 50 55	
25	acc agg cat gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca	336
	Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro	
	60 65 70	
30	tgc cca tgg cca atg att gag aaa tta cct tgt gct gcc ttg act gac	384
	Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp	
	75 80 85	
35	cga gaa tgc act tgc cca cct ggc atg ttc cag tct aac gct acc tgt	432
	Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys	
	90 95 100	
40	gcc ccc cat acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg	480
	Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly	
	105 110 115	
45	aca gag act gag gat gtg cgg tgt aag cag tgt gct cgg ggt acc ttc	528
	Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe	
	120 125 130 135	
50	tca gat gtg cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt	576
	Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys	
	140 145 150	
55	ctg agt cag aac ctg gtg gtg atc aag ccg ggg acc aag gag aca gac	624
	Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp	
	155 160 165	
60	aac gtc tgt ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc	672
	Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser	
	170 175 180	
65	cct ggc aca gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa	720
	Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu	
	185 190 195	
70	gtc cct tcc tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc	768
	Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser	
	200 205 210 215	

SubA2

	aac tct tct gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa	816
	Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu	
	220 225 230	
5	ggg aca gtc cct gac aac aca agc tca gca agg ggg aag gaa gac gtg	864
	Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val	
	235 240 245	
10	aac aag acc ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc	912
	Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro	
	250 255 260	
15	cac cac aga cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg	960
	His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly	
	265 270 275	
20	ggc gag aag tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct	1008
	Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro	
	280 285 290 295	
25	aga cag aac cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg	1056
	Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp	
	300 305 310	
30	atg att gtg ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg gtg tgc	1104
	Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys	
	315 320 325	
35	agt atc cgg aaa agc tgc agg act ctg aaa aag ggg ccc cgg cag gat	1152
	Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp	
	330 335 340	
40	ccc agt gcc att gtg gaa aag gca ggg ctg aag aaa tcc atg act cca	1200
	Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro	
	345 350 355	
45	acc cag aac cgg gag aaa tgg atc tac tac tgc aat ggc cat gga ccc	1248
	Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro	
	360 365 370 375	
50	cat gat gag gag tgg ggg ttg atg gag aga cat att caa gat att tat	1296
	His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr	
	380 385 390	
55	att caa aga agc aat caa gat tca gaa aga tgg ggt tgataatttt	1342
	Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly	
	395 400	
60	tacttcaccc tgggaggcag catagtgcag tgaaaggatat cgatatcctg aagctttag	1402
	cagcccaagt gggaagccag tggaaagata tctatcagtt tctttgcaat gccagtgaga	1462
	gggaggttgc tg	1474
	<210> 8	
	<211> 444	
	<212> PRT	
	<213> primate	

SubA2

<400> 8
Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

5 Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25 -20 -15 -10

Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
-5 -1 1 5

10 Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
15 25 30 35

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
40 45 50 55

20 Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
75 80 85

25 Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
90 95 100

Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
30 105 110 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
120 125 130 135

35 Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
140 145 150

Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
155 160 165

40 Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
170 175 180

Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
45 185 190 195

Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
200 205 210 215

50 Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
220 225 230

Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
235 240 245

55 Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
250 255 260

His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
60 265 270 275

SubA2

5 Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
280 285 290 295

Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
300 305 310

10 Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
315 320 325

Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
330 335 340

15 Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro
345 350 355

Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro
360 365 370 375

20 His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr
380 385 390

Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly
395 400

25

<210> 9
<211> 227
<212> PRT
30 <213> rodent

<400> 9
Met Ala Pro Ala Ala Leu Trp Val Ala Leu Val Phe Glu Leu Gln Leu
1 5 10 15

35 Trp Ala Thr Gly His Thr Val Pro Ala Gln Val Val Leu Thr Pro Tyr
20 25 30

Lys Pro Glu Pro Gly Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp
35 40 45

Arg Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val
50 55 60

45 Lys His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu
65 70 75 80

Ala Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser
85 90 95

50 Cys Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr
100 105 110

Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala
115 120 125

55 Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys
130 135 140

60 Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn

Sub A2

MURPHY, et al.

100

SF0818K

145 150 155 160
Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser
165 170 175
5 Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile
180 185 190
10 Pro Gly Asn Ala Ser Thr Asp Ala Val Cys Ala Pro Glu Ser Pro Thr
195 200 205
Leu Ser Ala Ile Pro Arg Thr Leu Tyr Val Ser Gln Pro Glu Pro Thr
210 215 220
15 Arg Ser Gln
225
20 <210> 10
<211> 225
<212> PRT
<213> primate
25 <400> 10
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1 5 10 15
Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30
30 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60
35 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
40 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110
45 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
50 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
55 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
60

SubA2

MURPHY, et al.

101

SF0818K

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220

Gln
225

<210> 11
<211> 187
<212> PRT
<213> primate

<400> 11
Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
1 5 10 15

Lys, Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly
180 185

<210> 12
<211> 636
<212> DNA
<213> rodent

<220>
<221> CDS

<222> (104)..(553)

<220>

<221> mat peptide

<222> (191)..(553)

<400> 12

ggcagcaggg cgtttggcgc ggaagtgcta ccaagctgcg gaaagcgtga gtctggagca 60

cagcactggc gactagcagg aataaacacg tttggtgaga gcc atg gca ctc aag 115
Met Ala Leu Lysgtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc cta 163
Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe Leu
-25 -20 -15 -10ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg cag 211
Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg Gln
-5 -1 1 5cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag tgc 259
Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln Cys
10 15 20gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg gag 307
Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu
25 30 35gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac tgg 355
Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp Trp
40 45 50 55ggc ttc cag aag tgt aag cca tgt ggc gac tgt ggc ctg gtg aac cgc 403
Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn Arg
60 65 70ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg gac 451
Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly Asp
75 80 85tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa gac 499
Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp
90 95 100atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca cac 547
Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro His
105 110 115tgt gag tgatgtgcca agtggcagca gacctttaa aaaaaaagaa aaaaaaacia 603
Cys Glu
120

acaaaaacia aaaaaaaaaa aaaaaaaaaa aaa 636

<210> 13

<211> 150

<212> PRT

<213> rodent

Sub A2

MURPHY, et al.

103

SF0818K

<400> 13

Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
-25 -20 -15

5 Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
-10 -5 -1 1

10 Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
5 10 15

Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
20 25 30 35

15 Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
40 45 50

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
55 60 65

20 Leu, Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
70 75 80

Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
85 90 95

25 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
100 105 110 115

30 Tyr Glu Pro His Cys Glu
120

<210> 14

<211> 474

35 <212> DNA

<213> primate

<220>

<221> CDS

40 <222> (78)..(473)

<220>

<221> misc_feature

<222> (308)

45 <223> N at 308, 315, 333, 412, 431, 436, 444, and 473 may be A, C, G, or
T; translated amino acid depends on genetic code

<400> 14

50 cgcgctgagg tggatttgta cggagtcgcc atttgggagc aagagccatc tactcgtccg 60

ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
1 5 10

55 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
15 20 25

60 tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206

SubA2

MURPHY, et al.

104

SF0818K

Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
 30 35 40
 5 tgc cct cct cgc agt aca aaa gca gct ggg gcc acc aca aat gtc aga 254
 Cys Pro Pro Arg Ser Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg
 45 50 55
 10 gtt gca tca cct gtg ctg tca tca atc gtg ttc aga agg ttc aac tgc 302
 Val Ala Ser Pro Val Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys
 60 65 70 75
 15 aca gtn acc tct nat gct gtc tgt ggg gga ngg ttt gcc caa gtt tct 350
 Thr Xaa Thr Ser Xaa Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser
 80 85 90
 20 aac cga aag aca cgc cat tgg aag gct gcc agg acc aag gat ggc atc 398
 Asn Arg Lys Thr Arg His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile
 95 100 105
 25 ccg tgg cac aaa gnc aga ccc cca act tct gan ggt tnc aaa gtg nct 446
 Pro Trp His Lys Xaa Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa
 110 115 120
 30 ttc caa ttg gag ctt aat ggg agg can a 474
 Phe Gln Leu Glu Leu Asn Gly Arg Xaa
 125 130
 <210> 15
 <211> 132
 <212> PRT
 <213> primate
 <400> 15
 35 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1 5 10 15
 40 Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
 20 25 30
 45 Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Ser
 35 40 45
 50 Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg Val Ala Ser Pro Val
 50 55 60
 55 Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys Thr Xaa Thr Ser Xaa
 65 70 75 80
 60 Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser Asn Arg Lys Thr Arg
 85 90 95
 His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile Pro Trp His Lys Xaa
 100 105 110
 Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa Phe Gln Leu Glu Leu
 115 120 125
 Asn Gly Arg Xaa
 130

Sub A2

5 <210> 16
<211> 546
<212> DNA
<213> primate

10 <220>
<221> CDS
<222> (78)..(308)

15 <220>
<221> misc_feature
<222> (317)
<223> N at 317, 340, 351, 389, 398, 428, 429, 433, 452, 468, 483, 534,
and 541 may be A, C, G, or T

20 <400> 16
cgcgctgagg tggatttgta cggaggtccc atttgggagc aagagccatc tactcgtccg 60
ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
1 5 10

25 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
15 20 25

30 tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
30 35 40

35 tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254
Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
45 50 55

40 agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc caa ctg 302
Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu
60 65 70 75

cac agc taacctctna tgctgtctgt ggggatgttt gncccaagtt ctnaccgaaa 358
His Ser

45 agacacgccca tgggaaggct ggcaggacca ngaatggccn tcccgtggca gaaagccaga 418
ccccccaacn nctgnagggt ccaatgtggc cttncatttt ggaagcttan tgggaaggca 478
gatgncaacc caaagtggcc ccttcaggga ggccaaaatt tgttggcaat gggtnagca 538

50 gcntgccca 546

55 <210> 17
<211> 77
<212> PRT
<213> primate

60 <400> 17
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val

SubA2

MURPHY, et al.

106

SF0818K

1 5 10 15

Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
20 25 30

5 Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
35 40 45

10 Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
50 55 60

Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu His Ser
65 70 75

15 <210> 18
<211> 932
<212> DNA
<213> primate

20 <220>
<221> CDS
<222> (78)..(770)

25 <220>
<221> misc_feature
<222> (782)
<223> N; may be A, C, G, or T

30 <400> 18
cgcgctgagg tggatttgta ccggagtcgc atttgggagc aagagccatc tactcgtccg 60

35 ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
1 5 10

40 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
15 20 25

45 tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala
30 35 40

50 tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254
Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
45 50 55

55 agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc aac tgc 302
Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys
60 65 70 75

60 aca gct acc tct aat gct gtc tgt ggg gac tgt ttg ccc agg ttc tac 350
Thr Ala Thr Ser Asn Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr
80 85 90

cga aag aca cgc att gga ggc ctg cag gac caa gag tgc atc ccg tgc 398
Arg Lys Thr Arg Ile Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys
95 100 105

SubA2

MURPHY, et al.

107

SF0818K

acg aag cag acc ccc acc tct gag gtt caa tgt gcc ttc cag ttg agc 446
 Thr Lys Gln Thr Pro Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser
 110 115 120

5 tta gtg gag gca gat gca ccc aca gtg ccc cct cag gag gcc aca ctt 494
 Leu Val Glu Ala Asp Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu
 125 130 135

10 gtt gca ctg gtg agc agc ctg cta gtg gtg ttt acc ctg gcc ttc ctg 542
 Val Ala Leu Val Ser Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu
 140 145 150 155

15 ggg ctc ttc ttc ctc tac tgc aag cag ttc ttc aac aga cat tgc cag 590
 Gly Leu Phe Phe Leu Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln
 160 165 170

20 cgt gga ggt ttg ctg cag ttt gag gct gat aaa aca gca aag gag gaa 638
 Arg Gly Gly Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu
 175 180 185

tct ctc ttc ccc gtg cca ccc agc aag gag acc agt gct gag tcc caa 686
 Ser Leu Phe Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln
 190 195 200

25 gtc tct tgg gcc cct ggc agc ctt gcc cag ttg ttc tct ctg gac tct 734
 Val Ser Trp Ala Pro Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser
 205 210 215

30 gtt cct ata cca caa cag cag cag ggg cct gaa atg tgatgtccac 780
 Val Pro Ile Pro Gln Gln Gln Gln Gly Pro Glu Met
 220 225 230

angagctaata accctacaga tggggcatat cctatcccat cccaccagag gattgattct 840

35 ccatttcaca aggactgata tggagcattt cttgcttccc tgttgtagtc tggggagcca 900

gattccacat tcatgggact accagacatg tt 932

40 <210> 19
 <211> 231
 <212> PRT
 <213> primate

45 <400> 19
 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1 5 10 15

50 Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
 20 25 30

Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
 35 40 45

55 Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
 50 55 60

60 Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
 65 70 75 80

SubA2

MURPHY, et al.

108

SF0818K

5
10
15
20
25
30

Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
85 90 95

Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
100 105 110

Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
115 120 125

Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
130 135 140

Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145 150 155 160

Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
165 170 175

Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
180 185 190

Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Trp Ala Pro
195 200 205

Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser Val Pro Ile Pro Gln
210 215 220

Gln Gln Gln Gly Pro Glu Met
225 230